GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 24, 2003, 10:59:02 ; Search time 11.364 Seconds
                                    (without alignments)
                                    1025.596 Million cell updates/sec

Title: US-09-508-849A-17
Perfect score: 1523
Sequence: 1 MQQPFNPYPQIYWVDSSAS...........SELSLVNFEESQTFFGLYKL 281

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1523	100.0	281	1	P48023	TNF6_HUMAN	homo sapien
2	1473.5	96.7	280	1	Q9bdn1	TNF6_CERTO	cercocebus
3	1469.5	96.5	280	1	Q9my16	TNF6_MACMU	macaca mula
4	1295.5	85.1	282	1	Q9bea8	TNF6_PIG	sus scrofa
5	1156	75.9	279	1	P41047	TNF6_MOUSE	mus musculu
6	1136.5	74.6	278	1	P36940	TNF6_RAT	rattus norv
7	250	16.4	239	1	Q9gyh9	TN14_MOUSE	mus musculu
8	224.5	14.7	240	1	O43557	TN14_HUMAN	homo sapien
9	205	13.5	202	1	O06332	TNFB_RAT	rattus norv
10	204	13.4	202	1	P09225	TNFB_MOUSE	mus musculu
11	202.5	13.3	205	1	Q9jm09	TNFB_MARMO	marmota mon
12	200.5	13.2	201	1	Q9xt48	TNFB_MACEU	macropus eu
13	200.5	13.2	291	1	P50592	TN10_MOUSE	mus musculu
14	200	13.1	197	1	P10154	TNFB_RABIT	oryctolagus
15	193.5	12.7	174	1	O95150	TN15_HUMAN	homo sapien
16	191	12.5	205	1	P01374	TNFB_HUMAN	homo sapien
17	189	12.4	317	1	O14788	TN11_HUMAN	h tumor nec
18	186.5	12.2	234	1	P29553	TNFA_HORSE	equus cabal
19	186	12.2	233	1	P51916	TNFA_TURTR	tursiops tr
20	186	12.2	281	1	P50591	TN10_HUMAN	homo sapien
21	185.5	12.2	232	1	P23563	TNFA_PIG	sus scrofa
22	185	12.1	233	1	O8wnr1	TNFA_DELLE	delphinapte
23	184	12.1	204	1	P26445	TNFB_PIG	sus scrofa
24	183.5	12.0	204	1	O06600	TNFA_BOVIN	bos taurus
25	183	12.0	233	1	O06599	TNFA_BOVIN	bos taurus
26	183	12.0	272	1	Q91dd8	TNF5_CHICK	gallus gall
27	181	11.9	233	1	P01375	TNFA_HUMAN	homo sapien
28	180	11.8	233	1	O35734	TNFA_MARMO	marmota mon
29	178	11.7	233	1	P79374	TNFA_TRIVU	trichosurus
30	177	11.6	141	1	P21260	YPRO_OWEFU	owenia fusi
31	177	11.6	233	1	P51742	TNFA_CANFA	canis famil
32	176	11.6	233	1	P33620	TNFA_PAPSP	papio sp. (
33	175.5	11.5	229	1	P51743	TNFA_CEREL	cervus elap
34	174	11.4	233	1	O77764	TNFA_MACEU	macropus eu
35	174	11.4	233	1	P48094	TNFA_MACMU	macaca mula
36	173.5	11.4	316	1	O35235	TN11_MOUSE	m tumor nec
37	172.5	11.3	318	1	Q9ese2	TN11_RAT	r tumor nec
38	171.5	11.3	415	1	P08001	ACRO_PIG	sus scrofa
39	171	11.2	233	1	P79337	TNFA_MACFA	macaca fasc
40	170	11.2	233	1	O77510	TNFA_PAPHU	papio hamad
41	169.5	11.1	485	1	P21997	SSGP_VOLCA	volvox cart
42	168.5	11.1	235	1	P04924	TNFA_RABIT	oryctolagus
43	166.5	10.9	234	1	P13296	TNFA_CAPHI	capra hircu
44	165.5	10.9	389	1	Q03173	NDPP_MOUSE	mus musculu
45	165	10.8	233	1	P19101	TNFA_FELCA	felis silve

ALIGNMENTS

RESULT 1
TNF6_HUMAN

ID   TNF6_HUMAN   STANDARD;   PRT;   281 AA.
AC   P48023; Q9B2P9;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN   TNFSF6 OR FASL OR APTLG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95127560; PubMed=7826947;
RA   Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT   "Human Fas ligand: gene structure, chromosomal location and species
RT   specificity.";
RL   Int. Immunol. 6:1567-1574(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95071350; PubMed=7980502;
RA   Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA   Fusamoto H., Kamada T.;
RT   "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT   infection.";
RL   Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=95105731; PubMed=7528780;
RA   Alderson M.;
RT   "Fas ligand mediates activation-induced cell death in human T
RT   lymphocytes.";
RL   J. Exp. Med. 181:71-77(1995).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Leukocyte;
RA   Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT   "Isolation and characterization of a new naturally occuring variant of
RT   human Fas ligand that is expressed only in membrane bound form.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Wilkinson J.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Blood;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

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RN   [8]
RP   SEQUENCE OF 1-10 FROM N.A.
RC   TISSUE=Blood;
RA   Matsumura M., Nakanishi Y., Ohba Y.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX   PubMed=9228058;
RA   Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA   Terskikh A., Peitsch M.C., Tschopp J.;
RT   "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL   J. Biol. Chem. 272:18827-18833(1997).
RN   [10]
RP   PROCESSING.
RX   PubMed=9427603;
RA   Tanaka M., Itai T., Adachi M., Nagata S.;
RT   "Downregulation of Fas ligand by shedding.";
RL   Nat. Med. 4:31-36(1998).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects.
CC   -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC       INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC       SURFACE.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2;
CC       are produced by alternative splicing.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC       lymphoproliferative syndrome (ALPS), also known as Canale-Smith
CC       syndrome (CSS), a childhood syndrome involving hemolytic anemia
CC       and thrombocytopenia with massive lymphadenopathy and
CC       splenomegaly.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/33387696674-g.htm".
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X89102; CAA61474.1; -.
DR   EMBL; U08137; AAC50071.1; -.
DR   EMBL; U11821; AAC50124.1; -.
DR   EMBL; D38122; BAA07320.1; -.
DR   EMBL; AF288573; AAG60017.1; -.
DR   EMBL; Z96050; CAB09424.1; -.
DR   EMBL; BC017502; AAH17502.1; -.
DR   EMBL; AB013303; BAA32542.1; -.
DR   HSSP; P01375; 1TNF.
DR   Genew; HGNC:11936; TNFSF6.
DR   MIM; 134638; -.
DR   MIM; 601859; -.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW   Alternative splicing; Antigen.
FT   CHAIN         1    281       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, MEMBRANE FORM.
FT   CHAIN       130    281       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, SOLUBLE FORM.
FT   DOMAIN        1     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    102       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      103    281       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     70       PRO-RICH.
FT   DOMAIN       45     65       POLY-PRO.
FT   SITE        129    130       CLEAVAGE.
FT   DISULFID    202    233       POTENTIAL.
FT   CARBOHYD    184    184       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    117    127       STSQMHTASSL -> ATPVHPLKKRS (IN ISOFORM
FT                                2).
FT   VARSPLIC    128    281       MISSING (IN ISOFORM 2).
FT   MUTAGEN     206    206       P->D,F,R: LOWERS BINDING TO TNFRSF6
FT                                AND REDUCES CYTOTOXITY MORE THAN A
FT                                HUNDREDFOLD.
FT   MUTAGEN     218    218       Y->F,R: LOWERS BINDING TO TNFRSF6 AND
FT                                ABOLISHES CYTOTOXITY.
FT   MUTAGEN     275    275       F->L: ABOLISHES BINDING TO TNFRSF6 AND
FT                                CYTOTOXICITY.
SQ   SEQUENCE   281 AA;  31485 MW;  A8ACEB3582465B9BB CRC64;
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Query Match             100.0%;  Score 1523;  DB 1;  Length 281;
Best Local Similarity   100.0%;
Matches 281;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPLPPPPP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPLPPPPP 60

Qy         61 PPLPLPLPPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PPLPLPLPPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ 120
              (*)
Qy        121 MHTASSLEKQIGHPSPPPEEKKELRKVAHLTGKSNSRSMPLEWEDTGIVLLSGVKYKKGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTGIVLLSGVKYKKGG 180

Qy        181 LVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKKMMSYCTTGQMWA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LVINETGLYFVYSKVYFRGQSCNNLPLSHKYVMRNSKYPQDLVMMEGKKMMSYCTTGQMWA 240

Qy        241 RSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
              |||||||||||||||||||||||||||||||||||||||||
Db        241 RSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
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RESULT 2
TNF6_CERTO
ID   TNF6_CERTO              STANDARD;      PRT;      280 AA.
AC   Q9BDN1;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (CD95L protein).
GN   TNFSF6 OR FASL OR CD95L.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
```

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RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; AF344847; AAK37606.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT   CHAIN         1    280       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                               MEMBER 6, MEMBRANE FORM.
FT   CHAIN       129    280       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                               MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    101       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN      102    280       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     69       PRO-RICH.
FT   DOMAIN       45     64       POLY-PRO.
FT   SITE        128    129       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    201    232       POTENTIAL.
FT   CARBOHYD    183    183       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    259    259       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE  280 AA;  31407 MW;  729EA6067B7D398 CRC64;

Query Match  96.7%;  Score 1473.5;  DB 1;  Length 280;
Best Local Similarity  97.5%;  Pred. No. 7.2e-94;
Matches  274;  Conservative  0;  Mismatches  6;  Indels  1;  Gaps  1;

Qy    1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRREGCGORRPPPPPPPPPLPPPPP   60
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||||
Db    1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGCQRRPPPPPPPPPL-PPPPP   59

Qy   61 PPLPLPLPPLPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGNMFQLFHLQKELAELRESTSQ 120
        |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   60 PPLPLPLPPLPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ 119

Qy  121 MHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGG 180
        |||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||||
Db  120 KHTASSLEKQIGHPSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLLSGVKYKKGG 179

Qy  181 LVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA 240
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  180 LVINETGLYFVYSKVYFRGQSCTNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA 239

Qy  241 RSSYLGAVFNLTSADLYVNVSELSLVNFEESQTFFGLYKL 281
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        |||||||||||| ||||||||||||||||||||||||||||
Db  240 HSSYLGAVFNLTSDHLYVNVSELSLVNFEESQTFFGLYKL 280

RESULT 3
TNF6_MACMU
ID   TNF6_MACMU    STANDARD;    PRT;    280 AA.
AC   Q9MYL6; Q9BDM5;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE   (CD95L protein).
GN   TNFSF6 OR FASL OR CD95L.
OS   Macaca mulatta (Rhesus macaque),
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544, 9541, 9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.fascicularis, and M.nemestrina;
RA   Kirii Y., Inoue T., Yoshino K.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -----------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; AF344856; AAK37539.1; -.
DR   EMBL; AB035138; BAA90294.1; -.
DR   EMBL; AB035139; BAA90295.1; -.
DR   EMBL; AB035140; BAA90296.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT   CHAIN         1    280       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                               MEMBER 6, MEMBRANE FORM.
```

```
FT   CHAIN       129    280       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     80       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     81    101       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      102    280       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     69       PRO-RICH.
FT   DOMAIN       45     64       POLY-PRO.
FT   SITE        128    129       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    201    232       POTENTIAL.
FT   CARBOHYD    183    183       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    259    259       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CONFLICT     60     60       S -> P (IN REF. 1).
SQ   SEQUENCE    280 AA;  31367 MW;  F0B284D61A132EB4 CRC64;

Query Match                96.5%;   Score 1469.5;  DB 1;  Length 280;
Best Local Similarity      97.5%;   Pred. No.1.4e-93;
Matches  274;  Conservative    0;  Mismatches    6;  Indels     1;  Gaps     1;

Qy      1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPLPPPPP 60
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      1 MQQPFNYPYPQIFWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPL-PPPPP 59

Qy     61 PPLPLPLPPLPPLKKRGNHSTGLCLLVMFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 SPLPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ 119

Qy    121 MHTASSLEKQIGHPSPPPEKKELRVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 KHTASSLEKQIGHPSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLLSGVKYKKGG 179

Qy    181 LVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 LVINETGLYFVYSKVYFRGQSCTNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA 239

Qy    241 RSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
          ||||||||||||||||||||||||||||||||||||||||
Db    240 HSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 280
```

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RESULT 4
ID   TNF6_PIG     STANDARD;    PRT;    282 AA.
AC   Q9BEA8; Q95N10; Q95M04;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE   ligand).
GN   TNFSF6 OR FASL.
OS   Sus scrofa (Pig).
OG   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21322533; PubMed=11429161;
RA   Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT   "Molecular cloning, characterization, and expression of porcine Fas
RT   ligand (CD95 ligand).";
RL   J. Interferon Cytokine Res. 21:305-312(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Guanxi bama miniature pig;
RA   Zhu N., Young Y.;
RT   "Molecular cloning and characterizaion of porcine Fas ligand cDNA.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RA   Tsuyuki S., Kono M., Bloom E.T.;
RT   "Cloning and potential utility of porcine Fas ligand: overexpression
```

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RT   in porcine cells protects them from attack by human cytolytic cells.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
RX   PubMed=11792426;
RA   Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT   "Porcine Fas-ligand gene: genomic sequence analysis and comparison
RT   with human gene.";
RL   Mol. Immunol. 38:581-586(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- INDUCTION: By IL-18.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB027297; BAB40919.1; -.
DR   EMBL; AY033634; AAK56449.1; -.
DR   EMBL; AF397407; AAK84408.1; -.
DR   EMBL; AB069764; BAB64291.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR000478; TNF_abc.
DR   InterPro; IPR003636; TNF_abc.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS00049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT   CHAIN       131    282       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, MEMBRANE FORM.
FT   CHAIN         1    282       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      104    282       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     70       PRO-RICH.
FT   DOMAIN       45     56       POLY-PRO.
FT   SITE        130    131       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    203    234       POTENTIAL.
FT   CARBOHYD    185    185       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    251    251       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    261    261       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CONFLICT      5      5       F -> L (IN REF. 4).
FT   CONFLICT     57     57       T -> L (IN REF. 2).
FT   CONFLICT     57     57       T -> P (IN REF. 2).
SQ   SEQUENCE    282 AA;  31756 MW;  6743DAA114567LFB CRC64;

Query Match                85.1%;   Score 1295.5;  DB 1;  Length 282;
Best Local Similarity      85.5%;   Pred. No.9.8e-82;
Matches  242;  Conservative   14;  Mismatches   24;  Indels     3;  Gaps     2;

Qy      1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPLPPPP-- 58
          |||||||||||||:||:||||||||||||:||| ||| ||| |||||||||||| ||||
Db      1 MQQPFNYPQIFWVDSSATSPWASPGSVPFCPASVPGRCQRRPPPPPPPPPPPP-PPPTLL 59
```

Qy   59 PPPLPLPPLPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRPST 118
          | ||||||| ||| :|| :|||||||||||||||||||||||||||||||||||||||| ||||
Db   60 PSRPLPLPPPSLKKRDHNAGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELTELRESA 119

Qy   119 SQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKK 178
          ||| ||||||||||||||||||||||||||||||||| :|||||| |:|||||||| |
Db   120 SORHTESSLEKQIGHPNLPSEKKELRKVAHLTGKPNSRSIPLEWEDTYGIALVSGVKYMK 179

Qy   179 GGLVINETGLYFVYSKVYFRGQSCNNLPLSHKYMRNSKYPQDLVMMEGKMMSYCTTTGQM 238
          |||||||||||||||||||||||||||||||||||||:||||| |||||||||||||||||
Db   180 GSLVINDTGLYFVYSKVYFRGQYCNNQPLSHKVYTRNSRYPQDLVMEGKMMNYCTTTGQM 239

Qy   239 WARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
          |||||||||||||||||||||||||||||||||| |||||||
Db   240 WARSSYLGAVFNLTSADHLYVNVSELSLVNFEESKTFFGLYKL 282

RESULT 5
ID   TNF6_MOUSE   STANDARD;   PRT;   279 AA.
AC   P41047; Q61217; Q9R1F2;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE   ligand).
GN   TNFSF6 OR FASL OR APT1LG1 OR GLD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM FASL).
RC   MEDLINE=94185175; PubMed=7511063;
RA   Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA   Suda T., Nagata S.;
RT   "Generalized lymphoproliferative disease in mice, caused by a point
RT   mutation in the Fas ligand.";
RL   Cell 76:969-976(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC   STRAIN=C57BL/6;
RC   MEDLINE=95380076; PubMed=7544870;
RA   Peitsch M.J., Tschopp J.J.;
RT   "Comparative molecular modelling of the Fas-ligand and other members
RT   of the TNF family.";
RL   Mol. Immunol. 32:761-772(1995).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM FASL).
RC   MEDLINE=95196085; PubMed=7889405;
RA   Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA   Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT   "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT   TNF family gene cluster.";
RL   Immunity 1:131-136(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM FASL).
RC   STRAIN=BALB/c;
RA   Fenner M.H., Shioda T., Isselbacher K.J.;
RT   "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT   two amino acids.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM FASLS).
RC   STRAIN=C3H; TISSUE=Spleen;
RC   MEDLINE=20021694; PubMed=10552956;
RA   Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
RA   Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT   "Cloning and expression of a short Fas ligand: A new alternatively
RT   spliced product of the mouse Fas ligand gene.";
RL   Blood 94:3456-3467(1999).
RN   [6]
RP   CHARACTERIZATION OF VARIANT GLD.
RC   MEDLINE=96091792; PubMed=7495745;
RA   Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
RA   Rousseau M., Bron C., Renno T., French L., Tschopp J.;
RT   "Characterization of the non-functional Fas ligand of gld mice.";
RL   Int. Immunol. 7:1381-1386(1995).
RN   [7]
RP   VARIANTS ALA-184 AND GLY-218.
RC   STRAIN=Various;
RC   PubMed=9108079;
RA   Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA   Yagita H.;
RT   "Polymorphism of murine Fas ligand that affects the biological
RT   activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC   transduces the apoptotic signal into cells. May be involved in
CC   cytotoxic T cell mediated apoptosis and in T cell development.
CC   TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC   peripheral tolerance, in the antigen-stimulated suicide of mature
CC   T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC   modulates its effects (By similarity).
CC   -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
CC   Secreted (isoforms FASL and FASLS).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: FASL (SHOWN HERE) AND FASLS; ARE
CC   PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
CC   WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
CC   INTERACTION.
CC   -!- PTM: The soluble form derives from the membrane form by
CC   proteolytic processing (By similarity).
CC   -!- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
CC   LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
CC   RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U06948; AAA17800.1; -.
DR   EMBL; U10984; AAA19778.1; -.
DR   EMBL; S76752; AAB33780.1; -.
DR   EMBL; U58995; AAB02915.1; -.
DR   EMBL; AF119335; AAD52106.1; -.
DR   HSSP; P01375; 4TSV.
DR   MGD; MGI:99255; Tnfsf6.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRODom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW   Disease mutation; Polymorphism; Alternative splicing.
FT   CHAIN   1   279   TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT   MEMBER 6, MEMBRANE FORM.
FT   CHAIN   128   279   TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT   MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN   1   78   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   79   100   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT   (POTENTIAL).
FT   DOMAIN   101   279   EXTRACELLULAR (POTENTIAL).
FT   DOMAIN   4   69   PRO-RICH.
FT   DOMAIN   45   51   POLY-PRO.
FT   SITE   127   128   CLEAVAGE (BY SIMILARITY).
FT   DISULFID   200   231   POTENTIAL.
FT   CARBOHYD   117   117   N-LINKED (GlcNAc...) (POTENTIAL).

Column 1

```
FT   CARBOHYD    182    182    N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD    248    248    N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD    258    258    N-LINKED (GLCNAC...)    (POTENTIAL).
FT   VARSPLIC      1    210    MISSING (IN ISOFORM FASLS).
FT   VARIANT     184    184    T -> A (IN STRAINS BALB/C AND DBA;
FT                             ENHANCES CYTOTOXICITY).
FT   VARIANT     218    218    E -> G (IN STRAINS BALB/C AND DBA;
FT                             ENHANCES CYTOTOXICITY).
FT   VARIANT     273    273    F -> L (IN GLD; ABOLISHES BINDING OF FASL
FT                             TO ITS RECEPTOR).
SQ   SEQUENCE    279 AA;  31442 MW;  37972E2728E0A1CA CRC64;
```

Query Match   75.9%; Score 1156; DB 1; Length 279;
Best Local Similarity 77.3%; Pred. No. 3.1e-72;
Matches 218; Conservative 25; Mismatches 35; Indels 4; Gaps 3;

```
Qy    1  MQQPFNYPYPQIYWDSSASSPWAPPGTVLPCPTSVPRRGQRRPPPPPPP-PLPPPP   59
         ||||:|||:|||:||||||:|||||||||||||||: || |||||||||||||| ||||||
Db    1  MQQPMNYPCPQIFWDSSSATSSWAPPGSVFPCPSCGPRGPGDQRRPPPPPPVSPLPPPSQ   60

Qy   60  PPPLPLPLPLPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTS  119
         ||:||  ||| ||||: :|||| ||:||||||||||||:|||||:|||||||||||||:
Db   61  PLPLP--PLPPLKKK-DHNTNLWLPVFFMVLVALVGMGLGMYQLFHLQKELAELREFTN   117

Qy  120  QMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKG  179
         | ::|||:|||||.|||.|:|||| |:||||||:|||||||||||||||| :|:|||||||
Db  118  QSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALISGVKYKKG  177

Qy  180  GLVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVNMEGKMMSYCTTGQMW  239
         |||||||||||||||||||||||||| ||.:|||||||||:|||| |||: ||||||||:|
Db  178  GLVINETGLYFVYSKVYFRGQSCNNQPLNIKVYMRNSKYPEDLVLMEEKRLNYCTTGQIW  237

Qy  240  ARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL  281
         | ||:||||||||||||||||||:||:||||||||:||||||||
Db  238  AHSSLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL   279
```

RESULT 6

```
ID   TNF6_RAT     STANDARD;      PRT;   278 AA.
AC   P36940;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE   ligand).
GN   TNFSF6 OR FASL OR APT1LG1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
```

[1]
SEQUENCE FROM N.A.
MEDLINE=94084792; PubMed=7505205;
Suda T., Takahashi T., Golstein P., Nagata S.;
"Molecular cloning and expression of the Fas ligand, a novel member
of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).

```
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects.
CC   -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC       THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC       KIDNEY AND LUNG.
CC   -!- INDUCTION: BY PMA/IONOMYCIN AND CONCANAVALIN/INTERLEUKIN-2.
CC   -!- PTM: The soluble form derives from the membrane form by
```

Column 2

```
CC        proteolytic processing (by similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U03470; AAC52129.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT   CHAIN         1    278    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                            MEMBER 6, MEMBRANE FORM.
FT   CHAIN       127    278    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                            MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT   DOMAIN        1     77    CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78     99    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                            (POTENTIAL).
FT   DOMAIN      100    278    EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        4     69    PRO-RICH.
FT   DOMAIN       45     58    POLY-PRO.
FT   SITE        126    127    CLEAVAGE (BY SIMILARITY).
FT   DISULFID    199    230    POTENTIAL.
FT   CARBOHYD    116    116    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    247    247    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    257    257    N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    278 AA;  31140 MW;  2898E18A862CEAC6 CRC64;
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Query Match   74.6%; Score 1136.5; DB 1; Length 278;
Best Local Similarity 76.6%; Pred. No. 6.6e-71;
Matches 216; Conservative 21; Mismatches 40; Indels 5; Gaps 3;

```
Qy    1  MQQPFNYPYPQIYWDSSASSPWAPPGTVLPCPTSVPRRGQRRPPPPPPP-PLPPPP   59
         ||||:|||:|||:||||||:|| |||||||||||||: || |||||||||||||| ||||||
Db    1  MQQPVNYPCPQIYWDSSSATSPWAPPGSVFSCPSSGPRGPGQRRPPPPPPPPSPLPPPSQ  60

Qy   60  PPPLPLPLPLPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTS  119
         ||:|||| ||| |||:: ||||| ||:||||||||||||:||||:||||||||||||||:
Db   61  PPPLP--PLSPLKKKDN--IELWLPVIFFMVLVALVGMGLGMYQLFHLQKELAELREFTN  116

Qy  120  QMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKG  179
         | ::|||:|||.:|||.|:|:|||| |:||||:|||||||||||||||| :|:|||||||
Db  117  HSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLEWEDTYGTALISGVKYKKG  176

Qy  180  GLVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVNMEGKMMSYCTTGQMW  239
         |||||: |||||||||||||||||| ||.:|||||||:||:|||| ||||: ||||||||
Db  177  GLVINEAGLYFVYSKVYFRGQSCNSQPLSHKVYMRNFKYPGDLVLMEEKRLNYCTTGQIW  236

Qy  240  ARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL  281
         | ||:||||||||||||||||||:||:||||||||:||||||||
Db  237  AHSSLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL   278
```

RESULT 7

```
ID   TN14_MOUSE   STANDARD;      PRT;   239 AA.
AC   Q9QYH9;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 14.
GN   TNFSF14 OR LIGHT.
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=10700230;
RA   Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D.,
RA   Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.;
RT   "Modulation of T-cell-mediated immunity in tumor and graft-versus-host
RT   disease models through the LIGHT co-stimulatory pathway.";
RL   Nat. Med. 6:283-289(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Misawa K., Nosaka T., Kitamura T., Kojima T.;
RT   "Murine LIGHT, a homologue of human LIGHT which is a member of TNF
RT   family.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoma;
RA   Force W.R., Todd P.K., Mikayama T.;
RT   "Mouse LIGHT: molecular genetics, ligand binding and expression.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!-  FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
     decoy receptor TNFRSF6B modulates its effects. Activates NFKB
     and stimulates the proliferation of T cells.
-!-  SUBUNIT: Homotrimer (By similarity).
-!-  SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
     similarity).
-!-  PTM: The soluble form derives from the membrane form by
     proteolytic processing.
-!-  SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
```

```
DR   EMBL; AF123385; AAF76453.1; -.
DR   EMBL; AB029155; BAA88559.1; -.
DR   EMBL; AF227533; AAF36722.1; -.
DR   MGD; MGI:1355317; Tnfsf14.
HSSP; P01375; 4TSV.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT   CHAIN         1    239       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 14, MEMBRANE FORM.
FT   CHAIN       282    239       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 14, SOLUBLE FORM.
FT   DOMAIN        1     37       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     38     58       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       59    239       EXTRACELLULAR (POTENTIAL).
FT   SITE         81     82       CLEAVAGE (POTENTIAL).
FT   DISULFID    152    187       POTENTIAL.
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   239 AA;  26638 MW;  217874AC71AD6BE3 CRC64;
```

```
Query Match             16.4%;  Score 250;  DB 1;  Length 239;
Best Local Similarity   30.6%;  Pred. No. 1.4e-10;
Matches   72;  Conservative   40;  Mismatches  85;  Indels  38;  Gaps  10;

Qy   68 LPPLKKRGNHSTGLCLLVMFFMVLVALVGLGL---GMFQLFHLQKELAEL------RE 116
         : : ||   ||    : |||:|| |:|| |  :  ||:  | | | | :
Db   18 IPFFRLEQNHRRCGTVQVSLALVLLGAGLATQGWF-LLRLHQRLGIDIVAHLPDGGKG 76

Qy  117 STSQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSR---SMPLEWEDTGIVLLSG 173
         || :|   ||  || |     | ||  | |  |:| || |  : || ||  | |
Db   77 SWEKL-----IQDRSHQANP------AAHLTGANASLIGIGGPLLWETRLGLAFLRG 123

Qy  174 VKYKKGGLIVNETGLYFYVSKVYFRGQSC----NNLPLSHKVYMRNSKYPQDLVMMEGK 228
         |  |   |  || || | |   |  | |       | : || : :| | : ||
Db  124 LTYHDCALVTMEPGYIYTYVSKVQLQSGSVGCPQGLANGLPITHGLYKRTSRYPKELELVSR 183

Qy  229 MMSYC---TTGQMWARSSTLGAVFNLTSADHLIYNVSELSIVNFEE-SQFFGLY 279
         | |    ||||| |:|  |  | :       |:|||: :|: |   :|| ||
Db  184 -RSPCGRANSSRVWWDSSFLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFGAF 237
```

RESULT 8
TN14_HUMAN

```
ID   TN14_HUMAN     STANDARD;      PRT;   240 AA.
AC   O43557; O75476; Q96LD2; Q8WYP8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
DE   mediator-ligand) (HVEM-L).
GN   TNFSF14 OR LIGHT OR HVEML.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Liver;
RX   MEDLINE=98122340; PubMed=9462508;
RA   Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA   Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA   Ware C.F.;
RT   "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT   ligands for herpesvirus entry mediator.";
RL   Immunity 8:21-30(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=98438532; PubMed=9765287;
RA   Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA   Tan K.B., Dede K., Spampanato D., Silverman C., Hensley P.,
RA   DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA   Truneh A., Young P.R.;
RT   "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT   HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RT   growth.";
RL   J. Biol. Chem. 273:27548-27556(1998).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX   MEDLINE=21528948; PubMed=11673523;
RA   Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT   "Genomic characterization of LIGHT reveals linkage to an immune
RT   response locus on chromosome 19p13.3 and distinct isoforms generated
RT   by alternate splicing or proteolysis.";
RL   J. Immunol. 167:5122-5128(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!-  FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
     decoy receptor TNFRSF6B modulates its effects. Activates NFKB,
     stimulates the proliferation of T cells, and inhibits growth of
     the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
     virus.
-!-  SUBUNIT: Homotrimer.
-!-  SUBCELLULAR LOCATION: Type II membrane protein and secreted
```

Left column

```
CC    -!-   (isoform 1); Cytoplasmic (isoform 2).
CC    -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/LIGHT
CC          delta-TM; are produced by alternative splicing.
CC    -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC          FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC          TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC          AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC          NONHEMATOPOIETIC TUMOR LINES.
CC    -!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC    -!- PTM: N-glycosylated.
CC    -!- PTM: The soluble form of isoform 1 derives from the membrane
CC          form by proteolytic processing.
CC    -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC    -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC          frameshift in position 178.
```

```
DR   EMBL; AF036581; AAC39563.1; -.
DR   EMBL; AF064090; AAC25169.1; -.
DR   EMBL; AY028261; AAK26160.1; -.
DR   EMBL; BC018058; AAH18058.1; ALT_FRAME.
DR   HSSP; P01375; 4TSV.
     Genew; HGNC:11930; TNFSF14.
     MIM; 604520; -.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW   Alternative splicing.
FT   CHAIN         1    240
FT   CHAIN       783    240        TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                 MEMBER 14, MEMBRANE FORM.
FT   CHAIN            240          TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                 MEMBER 14, SOLUBLE FORM.
FT   TRANSMEM     38     58        CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        1     37        SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       59    240        EXTRACELLULAR (POTENTIAL).
FT   SITE         82     83        CLEAVAGE (POTENTIAL).
FT   DISULFID    154    187        POTENTIAL.
FT   CARBOHYD    102    102        N-LINKED (GlcNAc...).
FT   VARSPLIC     38     73        MISSING (IN ISOFORM 2).
FT   CONFLICT    120    120        L -> V (IN REF. 4).
FT   CONFLICT    214    214        E -> K (IN REF. 2).
SQ   SEQUENCE    240 AA;  26351 MW;  49D0BF67E1390B39 CRC64;
```

```
Query Match
Best Local Similarity   30.7%;
Matches   65;   Conservative   41;   Mismatches   69;   Indels   37;   Gaps   10;
                        Score 224.5;   DB 1;   Length 240;

Qy     90  VLVALVGLGLGMFQLFHLQKELAELRESTSQMHT------ASSLEKQIGHPSPPEKK--  141
               :||:  |:|||   |||      |:|                 |||
Db     42  LILILMGAGLAVQGWFLLQ-----LHWRLGEMVRLPDGPAGSWEQLI------QERRSH  90

Qy    142  ELRKVAHLTGKSNS---RSMPLEWEDTYGIVLLSGVRYKKGGLVINETGLYFVYSKVYFR  198
           |: |||| |||||   |: || ||||||||||||:|| ||||||||||||:|||||||
Db     91  EVNPAAHLTGANSLTGSGGPLMWETQLGLAFLRGLSYHDGALVVTKAGYYYIYSKVQLG   150

Qy    199  GQSCNNLPL------SHKYMRNSKYPQDLVMMEGKMMSYC-----TTGQMWARSSYLGAV  248
           || | |        |||:|   |  ||||     |||||||||||  |||||||||||
Db    151  GVGC--------PLGLASTTHGLYKRTPRYPEELELLVSQ-QSPCGRATSSSSRVWWDSSFLGGV  206

Qy    249  FNLTSADHLYVNVSELSLVNFEE-SQTFFGLY  279
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Right column

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Db     .  207  VHLEAGEEVVVRVLDERLVRLRDGTRSYFGAF  238
```

```
RESULT 9
TNFB_RAT

ID   TNFB_RAT      STANDARD;    PRT;   202 AA.
AC   Q06332;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   LTA OR TNFSF1 OR TNFB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=94040766; PubMed=8224868;
RA   Kwon J., Chung I.Y., Benveniste E.N.;
RT   "Cloning and sequence analysis of the rat tumor necrosis
RT   factor-encoding genes.";
RL   Gene 132:227-236(1993).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer; and heterotrimer of either two LTA and one
CC       LTB subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
CC       protein (heterotrimers) (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
```

```
DR   EMBL; L00981; AAA16276.1; -.
DR   PIR; JN0869; JN0869.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     33        BY SIMILARITY.
FT   CHAIN        34    202        LYMPHOTOXIN-ALPHA.
FT   CARBOHYD     94     94        N-LINKED (GlcNAc...) (POTENTIAL).
SQ   SEQUENCE    202 AA;  22111 MW;  A56963CE33AE0C08 CRC64;
```

```
Query Match            13.5%;
Best Local Similarity  32.9%;
Matches   51;   Conservative   27;   Mismatches   67;   Indels   10;   Gaps   2;
                       Score 205;   DB 1;   Length 202;

Qy    137  PPEKK-----ELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVRYKKGGLVINETGLYFV  192
           |::|      |||||||:||:|   ::  |::||||||||||||:|||||||||:||||:|
Db     48  PPQKHLTHGLLKPAAHLVGYPSKQNSLLWRANTDRAFLRHGFSLNNNSLLIPTSGLYFV   107

Qy    193  SKVYFRGQSCN-----NLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLG  246
           :||  :   :  ::||  | | |||| ||  |  |||||||||||
Db    193  ...
```

```
Db        108  SQVFSGGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLLSAQKSVYPGLQGPWVRSMYQG  167
Qy        247  AVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL  281
               |||:|: |:|     :|   ||| | : |:||| :
Db        168  AVFLLSKGDQLSTHTDGISHLHFSPSTVFFGAFAL  202
```

RESULT 10

```
ID   TNFB_MOUSE     STANDARD;      PRT;   202 AA.
AC   P09225;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
DE   LTA OR TNFSF1 OR TNFB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88067722; PubMed=3684584;
RA   Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT   "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT   (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RL   Nucleic Acids Res. 15:9083-9084(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87040736; PubMed=3490653;
RA   Nedospasov S.A., Hirt B., Shakhov A.N., Dobrynin V.N., Kawashima E.,
RA   Accolla R.S., Jongeneel C.V.;
RT   "The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin
RT   (TNF-beta) are tandemly arranged on chromosome 17 of the mouse.";
RL   Nucleic Acids Res. 14:7713-7725(1986).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87231097; PubMed=3588316;
RA   Gray P.W., Chen E., Tang W.-L., Ruddle N.;
RT   "The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.";
RL   Nucleic Acids Res. 15:3937-3937(1987).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87224127; PubMed=2884262;
RA   Li C.B., Gray P.W., Lin P.F., McGrath K.M., Ruddle F.H.,
RA   Ruddle N.H.;
RT   "Cloning and expression of murine lymphotoxin cDNA.";
RL   J. Immunol. 138:4496-4501(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87252204; PubMed=2885372;
RA   Gardner S.M., Mock B.A., Hilgers J., Huppi K.E., Roeder W.D.;
RT   "Mouse lymphotoxin and tumor necrosis factor: structural analysis of
RT   the cloned genes, physical linkage, and chromosomal position.";
RL   J. Immunol. 139:476-483(1987).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA   Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 6-202 FROM N.A.
RX   MEDLINE=89144562; PubMed=3147435;
RA   Well D., Dautry F.;
RT   "Induction of tumor necrosis factor-alpha and -beta and
RT   interferon-gamma mRNA by interleukin 2 in murine lymphocytic cell
RT   lines.";
RL   Oncogene Res. 3:409-414(1988).
RN   [8]
RX   MEDLINE=91042516; PubMed=1700275;
RA   Well D., Brosset S., Dautry F.;
RT   "RNA processing is a limiting step for murine tumor necrosis factor
RT   beta expression in response to interleukin-2.";
RL   Mol. Cell. Biol. 10:5865-5875(1990).
-!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC   TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC   heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC   produced by lymphocytes and cytotoxic for a wide range of tumor
CC   cells in vitro and in vivo.
-!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC   LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC   similarity).
-!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
CC   protein (heterotrimers) (By similarity).
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   -------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------
DR   EMBL; U06950; AAA18593.1; -.
DR   EMBL; Y00467; CAA68529.1; -.
DR   EMBL; X06217; CAA29566.1; -.
DR   EMBL; X06218; CAA29567.1; -.
DR   EMBL; Y00137; CAA68330.1; -.
DR   EMBL; M16819; AAA40460.1; -.
DR   EMBL; M17015; AAA39450.1; -.
DR   EMBL; AF109719; AAC82485.1; -.
DR   EMBL; X14800; CAA32906.1; -.
DR   EMBL; M60586; AAA40461.1; -.
DR   PIR; B27303; B27303.
DR   PIR; S01342; S01342.
DR   PIR; S10083; S10083.
DR   HSSP; P01374; 1TNR.
DR   MGD; MGI:104797; Lta.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Cytotoxin; Signal.
FT   SIGNAL        1     33
FT   CHAIN        34    202       LYMPHOTOXIN-ALPHA.
FT   CARBOHYD     94     94       N-LINKED (GLCNAC...).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC...).
FT   CONFLICT    161    162       A -> P (IN REF. 5).
FT   CONFLICT    202    202       VR -> CG (IN REF. 2).
SQ   SEQUENCE   202 AA;  21998 MW;  F496F8C68S950D3 CRC64;

  Query Match             13.4%;  Score 204;  DB 1;  Length 202;
  Best Local Similarity   32.5%;
  Matches   51;  Conservative   25;  Mismatches   73;  Indels    8;  Gaps    2;

Qy        133  HPSPPPEKKE--LRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYF  190
               || ||::|::  ||:||:|| ::|:  : |  :|:|:| :::: | ::||:||:| |||:
Db         46  HPLFQKHLTHGILKPAAHLVGYPSKONSLLWRASTDRAFLRHGFSLSNNSLLIP?SGLYF  105

Qy        191  VYSKVYFRCQSCN------NLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGOMWARSSY  244
               ||| : |  ||||      ||:|:||: :  |:   :  : :  :  :|  ||:|| ||:|
Db        106  VYSQVVFSGGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLLSAQKSVYPGLQGPWVRSMY  165

Qy        245  LGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL  281
               :||||:|: |:|     :|   ||| | : |:||| :
Db        166  QGAVFLLSKGDQLSTHTDGISHLHFSPSTVFFGAFAL  202
```

RESULT 11

```
ID   TNFB_MARMO     STANDARD;      PRT;    205 AA.
AC   Q9JM09; Q9JM12;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   LTA OR TNFSF1 OR TNFB.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=20184748; PubMed=10721723;
RA   Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT   "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT   structure, characterization and biological activity.";
RL   Gene 242:295-305(2000).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTA and one
CC       LTB subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
CC       protein (heterotrimers) (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF096268; AAF34868.1; -.
DR   EMBL; AF095586; AAF34864.1; -.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR000478; TNF_abc.
DR   InterPro; IPR003636; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     34
FT   CHAIN        35    205       LYMPHOTOXIN-ALPHA.
FT   CARBOHYD     96     96       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     46     46       R -> W (IN REF. 1; AAF34864).
SQ   SEQUENCE   205 AA;  22229 MW;  EE1F8D84C04C8A7 CRC64;

Query Match             13.3%;
Best Local Similarity   30.0%;
Matches   70;  Conservative   36;  Mismatches   82;  Indels   45;  Gaps   11;

Qy    64 PP---LPLPLKKRGNHSTGLCLLVMFFMVLVAL---VGL-GLGMFQLFHLQKELAELRE 116
            ||  || | |:|  |:| |  | :||   ||     : ||  | |::|| :|| :|
Db     3 PPGRLYLPRVR------GTRLFLLIGLLLALPPRAKGLPGVGL-------------- 40

Qy   117 STSOMHTASSLEKOIGHGPSPPPEKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSGVK 175
            :|: |||||||||:|||||  :||||||||||||||||||||||| |:|||||||||
Db    41 ---LPSARAAQO--HPQKHFAHGTLKPAAHLVGDPSMON-SLRWRANTDRAFLRHGFS 93

Qy   176 YKKGGLVINETGLIFVISXVYFRGQSCNN-------LPLSHKVYMRNSKYPODLVMMEGKM 229
```

```
Db    94 LSNNSLLVPTSGLYFVYSQVVFSGEGCSSKKAVSTPLYLAHEVQLFSSQYPFHVPLLSAQ- 152

Qy   230 MSYCTTGQ-MWARSSLGAVFNLTSADHLIYNVSELSLVNFEESQTFGLYKL 281
            || :|   :  || | || ||:|:|  |  :: || :|: ||   ::| :||
Db   153 KSVCPGPQGPWVRSVYQGAVFLLTRGDQLSTHTDGISHLLFSPSSVFFGAFAL 205

RESULT 12
ID   TNFB_MACEU     STANDARD;      PRT;    201 AA.
AC   Q9XT48;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   LTA OR TNFSF1 OR TNFB.
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20284948; PubMed=10826697;
RA   Harrison G.A., Deane E.M.;
RT   "cDNA cloning of lymphotoxin alpha (LT-alpha) from a marsupial,
RT   Macropus eugenii (Tammar wallaby).";
RL   DNA Seq. 10:399-403(2000).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTA and one
CC       LTB subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
CC       protein (heterotrimers) (By similarity).
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF119336; AAD41773.1; -.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28    201       LYMPHOTOXIN-ALPHA.
FT   CARBOHYD     93     93       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   201 AA;  21536 MW;  8C4C3710B5091627 CRC64;

Query Match             13.2%;
Best Local Similarity   29.4%;
Matches   65;  Conservative   30;  Mismatches   87;  Indels   39;  Gaps   7;

Qy    78 STG-LCLLVMFFMVLVALVGLGIGMFQLFHLQKELAELRESTSQMHTASSLEKOIGHPSP 136
            ||  |||:||||:|:| :|| ||| |||||||:|:
Db     3 SSGVLCL-------------LGALSLQVLLLQPPGAQGAPNPDNSHSSS------PAP 41

Qy   137 PP-------EKKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSGVKYKKGGLVINE 185
```

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Db

Qy     42 PQTAQHLSQKSLKRETLKPAAHLVGDPDSVQD-SIHWRANTDHAFLRHGFSLSNNSLLVPT 100
          :::|  :::|  |||| :|  |  |  |::|  :: || ||:  |::   ::| ::  |::
Qy    186 TGLIYFVYSKVYFRGQSCNN-----LPLSHKYVMRNSKYPQDLVMMEGKMMSYCTTGQMWA 240
          ||:|||:||:|:|:  ||||     || ::||:|:| || || |:::| :|::  ::| ||
Db    101 SGLYFVYSQVVFSGASCSSEIPTPLLYLSHEVLLFSSKYQVHVPLLSAQKSVCSGTQGPWM 160

Qy    241 RSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
          :|| ||||||||||||||||||||||||||||||| | ||
Db    161 RSVYQGAVFLLTQGDRLSTYTDGVSHLLQSPSSVFFGAPAL 201
```

```
RESULT 13
ID     TN10_MOUSE          STANDARD;      PRT;     291 AA.
AC     P50592;
DT     01-OCT-1996 (Rel. 34, Created)
DT     01-OCT-1996 (Rel. 34, Last sequence update)
DT     15-JUN-2002 (Rel. 41, Last annotation update)
DE     Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE     apoptosis inducing ligand) (TRAIL protein).
GN     TNFSF10 OR TRAIL.
OS     Mus musculus (Mouse).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX     NCBI_TaxID=10090;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=96111955; PubMed=8777713;
RA     Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA     Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA     Goodwin R.G.;
RT     "Identification and characterization of a new member of the TNF
RT     family that induces apoptosis.";
RL     Immunity 3:673-682(1995).
CC     -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC         TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC         possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC         may be modulated by binding to the decoy receptors
CC         TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC         induce apoptosis.
CC     -!- SUBUNIT: HOMOTRIMER (By similarity).
CC     -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC     -!- TISSUE SPECIFICITY: WIDESPREAD.
CC     -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC     --------------------------------------------------------------------------
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CC     --------------------------------------------------------------------------
DR     EMBL; U37522; AAC52345.1; -.
DR     HSSP; P50591; 1D0G.
DR     MGD; MGI:1107414; Tnfsf10.
DR     InterPro; IPR003636; TNF_abc.
DR     InterPro; IPR000478; TNF_family.
DR     Pfam; PF00229; TNF; 1.
DR     ProDom; PD002012; TNF_abc; 1.
DR     SMART; SM00207; TNF; 1.
DR     PROSITE; PS00251; TNF_1; 1.
DR     PROSITE; PS50049; TNF_2; 1.
KW     Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT     DOMAIN        1     17       CYTOPLASMIC (POTENTIAL).
FT     TRANSMEM     18     38       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                  (POTENTIAL).
FT     DOMAIN       39    291       EXTRACELLULAR (POTENTIAL).
FT     CARBOHYD     52     52       N-LINKED (GLCNAC...) (POTENTIAL).
SQ     SEQUENCE   291 AA;   33477 MW;   3FEACAB9F0D7D802 CRC64;
```

```
Query Match             13.2%;       Score 200.5;      DB 1;    Length 291;
```

```
Best Local Similarity    28.3%;     Pred. No. 4.2e-07;
Matches    60;   Conservative   39;   Mismatches   68;   Indels   45;   Gaps    9;

Qy    103 QLFHLQKELAELRESTSQMHTASSLEKQLGHPSPSPPEEKELRKYAHLTG---KSNSRSMP 159
          |:|  :|:| | : :: :   | |  |::| :  || |   ||   :|       |||||:|
Db     87 QLYQLIEEVT-LR--TFQDISTVPEKQLSTPPLPRGGRPQKVAAHITGITRRSNSALIP 143

Qy    160 L---------EWEDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNL- 205
          :               ||  |::| |:|::|||::|  ||||:|||:|  |||||
Db    144 ISKPDGKTLGQKIESWESSRRGHSFLNHVLFRNGELVIEQEGLIYIYSQTYFRFQEAEDAS 203

Qy    206 ----------PLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWAR-------SSYLGA 247
                    :|  |: ||| : |:||:||:| |  ::|::|         : |  ||
Db    204 KMVSKDKVRFKQLVQYIY-KYTSYPDPIVLMKSARNS------CWSRDAEYGLYSIYQGG 256

Qy    248 VFNLTSADHLYVNVSELSLVNFEESQTFFGLY 279
          : |||||||:|:|| |||:| :|||:||  ||
Db    257 LFELKKNDRIFVSVTNEHLMDLDQEASFFGAF 288
```

```
RESULT 14
ID     TNFB_RABIT          STANDARD;      PRT;     197 AA.
AC     P10154;
DT     01-MAR-1989 (Rel. 10, Created)
DT     01-AUG-1991 (Rel. 19, Last sequence update)
DT     15-JUN-2002 (Rel. 41, Last annotation update)
DE     Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE     factor ligand superfamily member 1).
GN     LTA OR TNFSF1 OR TNFB.
OS     Oryctolagus cuniculus (Rabbit).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX     NCBI_TaxID=9986;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=90220566; PubMed=2633043;
RA     Shakhov A.N., Kuprash D.V., Turetskaya R.L., Azizov M.M.,
RA     Andreyeva A.V., Nedospasov S.A.;
RT     "Cloning and structural analysis of genes coding for tumor necrosis
RT     factor and lymphotoxin in rabbits.";
RL     Mol. Biol. (Mosk) 23:1743-1750(1989).
CC     -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC         TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC         heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC         produced by lymphocytes and cytotoxic for a wide range of tumor
CC         cells in vitro and in vivo.
CC     -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTA and one
CC         LTB subunits or (less prevalent) two LTA and one LTB subunits (By
CC         similarity).
CC     -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane
CC         protein (heterotrimers) (By similarity).
CC     -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC     --------------------------------------------------------------------------
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CC     --------------------------------------------------------------------------
DR     EMBL; X55745; CAA39275.1; ALT_SEQ.
DR     EMBL; M60340; AAA31483.1; -.
```

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DR   EMBL; M60341; AAA31485.1; -.
DR   PIR; JH0309; JH0309.
DR   PIR; PN0098; PN0098.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD000202; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS00049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Cytotoxin; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    197       LYMPHOTOXIN-ALPHA.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    197 AA;  21126 MW;  0CF18CC90B5E2345 CRC64;

Query Match             13.1%;  Score 200;  DB 1;  Length 197;
Best Local Similarity   26.0%;  Pred. No. 3e-07;
Matches    61;  Conservative  28;  Mismatches  82;  Indels  64;  Gaps   7;

Qy     55  PPPPPPPPPLPPLPPLPPLPLKKRGNHSTGICLLLVMFFMVLVALVGLGLGMFQLFHLQKELAEL 114
           ||||       ||::|::| |:
Db     19  PPPPGAQGLPGAEFPSAAR---------------------------------------- 38

Qy    115  RESTSQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSG 173
           |:| |||:| ::            |||||    ||   |:
Db     39  ------NAQQRLQKHFGHST------------LKPAAHLVGDPSAQD-SLRWRANTDRAFLRHG 83

Qy    174  VKYKKGGLVINETGLYFVYSKVYFRGQSCN-----NLPLSHKYYMRNSKYPQDLVMMEG 227
           | ::|||:||||::|: ||| | : || |       :|| | ::|  ::
Db     84  FSLSNNSLLVPSSGLYFVYSQVVFSGEGCSPKAVPTPLYLAHEVQLFSSQYSFHVPLLSA 143

Qy    228  KMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
           |     |  ||  |:||:|||||||:||:
Db    144  Q-KSVCPGPGPWVRSVYQGAVFLITQGDQLSTHTDGIAHLLSPSSVFFGAFAL 197
```

```
RESULT 15
TN15_HUMAN
ID   TN15_HUMAN   STANDARD;    PRT;   174 AA.
AC   O95150;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 15 (Vascular
DE   endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
GN   TNFSF15 OR VEGI OR TL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Umbilical vein;
RX   PubMed=98729042;
RA   Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
RA   Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
RA   Li L.-Y., Gentz R., Yu G.-L.;
RT   "VEGI, a novel cytokine of the tumor necrosis factor family, is an
RT   angiogenesis inhibitor that suppresses the growth of colon carcinomas
RT   in vivo.";
RL   FASEB J. 13:181-189(1999).
CC   -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
CC       (in vitro).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC       Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC       spleen, prostate, small intestine and colon.
CC   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
```

```
DR   EMBL; AF039390; AAD08783.1; -.
DR   Genew; HGNC:11931; TNFSF15.
DR   MIM; 604052; -.
DR   HSSP; P50591; 1D0G.
DR   InterPro; IPR003636; TNF_abc.
DR   InterPro; IPR000478; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD000202; TNF_abc; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT   DOMAIN        1     12       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     13     25       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       26    174       EXTRACELLULAR (POTENTIAL).
FT   DISULFID     85    125       POTENTIAL.
FT   CARBOHYD     56     56       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    174 AA;  20131 MW;  CCB83BA7E6673B98 CRC64;

Query Match             12.7%;  Score 193.5;  DB 1;  Length 174;
Best Local Similarity   36.8%;  Pred. No. 7.4e-07;
Matches    50;  Conservative  22;  Mismatches  49;  Indels  15;  Gaps   6;

Qy    160  LEWEDTYGIVLLSG-VKYKKGGLVINETGLYFVYSKVYFRGQS--CN------NLPLS 208
           || |   :  |:||::|||:||||:|:|| ||| | : ||   |        |||
Db     40  LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS 99

Qy    209  HKYYMR--NSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSL 266
           | :|    ||| |  |  :|  ||:| ||| | |:||:|||||||:||: |||:
Db    100  ITVVIIKVTDSYPEPTQQLLMG-TKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL 158

Qy    267  VNF-EESQTFFGLYKL 281
           :|| | ||| ||||
Db    159  VDYTKEDKTFFGAFLL 174
```

Search completed: June 24, 2003, 11:05:28
Job time : 11.364 secs

OM protein - protein search, using sw model

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Run on: June 24, 2003, 11:01:33 ; Search time 21.3505 Seconds
(without alignments)
1265.253 Million cell updates/sec

Title: us-09-508-849A-17
Perfect score: 1523
Sequence: 1 MQQPFNYPYPQIYWVDSSAS.............SELSLVNFEESQTFFGLYKL 281

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Database :   PIR_73:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1523	100.0	281	2	I38707	Fas ligand - human
2	1156	75.9	279	2	A53062	Fas ligand - mouse
3	1136.5	74.6	278	2	A49266	fas ligand - rat
4	205	13.5	202	1	JN0869	tumor necrosis fac
5	204	13.4	202	1	B27303	tumor necrosis fac
6	200	13.1	197	2	JH0309	tumor necrosis fac
7	191	12.5	205	1	QWHUX	lymphotoxin alpha
8	186.5	12.2	234	1	JQ1344	tumor necrosis fac
9	185.5	12.2	232	1	S12606	tumor necrosis fac
10	184	12.1	204	1	S17289	tumor necrosis fac
11	183.5	12.1	204	1	S24641	lymphotoxin - bovi
12	183	12.0	233	1	S24642	tumor necrosis fac
13	181	11.9	233	1	QWHUN	tumor necrosis fac
14	177	11.6	141	2	A34043	hypothetical proti
15	176	11.6	233	1	S22052	tumor necrosis fac
16	175	11.5	234	1	A25451	tumor necrosis fac
17	172	11.3	599	2	T10798	pherophorin-S - Vo
18	171.5	11.3	415	2	A34170	acrosin (EC 3.4.21
19	169.5	11.1	185	2	S52715	tumor necrosis fac
20	169.5	11.1	185	2	S52711	tumor necrosis fac
21	165.5	10.9	485	2	S27200	sulfated surface g
22	165	10.8	389	2	S11688	proline-rich prote
23	163.5	10.7	233	2	JH0529	tumor necrosis fac
24	163	10.7	234	2	S47538	tumor necrosis fac
25	162.5	10.7	1206	2	S24407	acrosin (EC 3.4.21
26	162.5	10.7	1468	2	S15515	formin isoform IV
27	161	10.6	193	2	S06192	formin - mouse
28	160	10.5	235	2	I54490	tumor necrosis fac
29	159.5	10.5	421	1	S11674	acrosin (EC 3.4.21
30	158.5	10.3	502	2	A55197	Wiskott-Aldrich sy
31	157	10.3	235	1	QWMSN	tumor necrosis fac
32	155.5	10.2	306	2	I49139	lymphotoxin-beta -
33	155.5	10.2	440	2	I49681	glyceraldehyde-3-p
34	154	10.1	235	2	JU0029	tumor necrosis fac
35	153	10.0	708	2	D96711	hypothetical prote
36	153	10.0	760	2	T06291	extension homolog T
37	152.5	10.0	1110	2	T19673	hypothetical prote
38	152	10.0	487	2	S42442	regulatory protein
39	151	9.9	196	2	B48232	nuclear protein EB
40	151	9.9	439	2	S51939	chitinase (EC 3.2.
41	151	9.9	980	2	S54986	cysteine-rich exte
42	151	9.9	1201	2	G84441	unknown protein [i
43	150.5	9.9	464	2	S22697	extension - Volvox
44	150.5	9.9	1255	2	T31065	diaphanous protein
45	149.5	9.8	645	2	A71416	hypothetical prote

ALIGNMENTS

RESULT 1
I38707
Fas ligand - human

C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: EMBL:U11821; NID:g995430; PIDN:AAC50124.1; PID:g995431
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X81102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
A;Genetics:
A;Gene: FasL
C;Genetics:
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1523; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-104;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MQQPFNYPYPQIYWVDSSASPWAPGTVLPCPTSVPRRPGQRRPPPPPPPPPPPLPPPPP 60

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A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein

Query Match             74.6%;  Score 1136.5;  DB 2;  Length 278;
Best Local Similarity   76.6%;  Pred. No. 2.8e-76;
Matches  216;  Conservative  21;  Mismatches  40;  Indels  5;  Gaps  3;

Qy    1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQORRPPPPPPPPLPPPPP   59
        ||||:||| ||:||||||: ::|| |||||:||| |  ||:|:||||||||||   | ||:
Db    1 MQQPVNYPCPQIYWVDSSATSPWAPPGSVFSCSGGSGPGPGQORRPPPPPPPPSPLPPPSQ  60

Qy   60 PPLPLP--PLTPLKKK-DHNINLWLLPVVFFMVLVALVGMGLGMYQLFHLQKELAELRESTS 117
Db   61 PLPLPLPPLKKRGNHSTGICLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTS   119

Qy  118 QSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALISGVKYKKG  177
Db  120 QMHTASSLEKQIGHPSPPEKKELRKVAHLTGKSNSRSRSMPLEWEDTYGIVLLSGVKYKKG  179

Qy  178 GLVINEAGLYFVYSKVYFRGQSCNNQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTTGQIW  237
Db  180 GLVINETGLYFYVSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMW  239

Qy  238 AHSSYLGAVFNLTSADHLIYVNISQLSLINFEESKIFFGLYKL  279
Db  240 ARSSYLGAVFNLTSADHLIYVNVSELSLVNFEESQTFFGLYKL  281
```

RESULT 2
A53062
fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

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Query Match             75.9%;  Score 1156;  DB 2;  Length 279;
Best Local Similarity   77.3%;  Pred. No. 1e-77;
Matches  218;  Conservative  25;  Mismatches  35;  Indels  4;  Gaps  3;

Qy    1 MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQORRPPPPPPPPLPPPPP   60
        ||||:||| ||:||||||  |:|| |||||:| |  ||: |:|||||||||    |||||
Db    1 MQQPMNYPCPQIFWVDSSATSSWAPPGSVFPCSGGPRGPDQORRPPPPPPPVSPLPPPSQ   59

Qy   61 PPLPLPLPPLKKRGNHSTGICLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQ  119
Db   60 PLPLP--PLTPLKKK-DHNINLWLLPVVFFMVLVALVGMGLGMYQLFHLQKELAELREFTN 117

Qy  120 QMHTASSLEKQIGHPSPPEKKELRKVAHLTGKSNSRSRSMPLEWEDTYGIVLLSGVKYKKG  179
Db  118 QSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALISGVKYKKG  177

Qy  181 LVINETGLYFYVSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA  240
Db  180 GLVINEAGLYFVYSKVYFRGQSCNNQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTTGQIW  236

Qy  241 RSSYLGAVFNLTSADHLIYVNVSELSLVNFEESQTFFGLYKL  281
Db  237 AHSSYLGAVFNLTSADHLIYVNISQLSLINFEESKIFFGLYKL  278
```

RESULT 3
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary

RESULT 4
JN0869
tumor necrosis factor beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0869
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A;Accession: JN0869
A;Molecule type: DNA
A;Residues: 1-202 <KWO>
A;Cross-references: GB:L00081; NID:g205253; PIDN:AAA16276.1; PID:g205255
A;Gene: TNF-beta
A;Genetics:
C;Introns: 32/3; 66/1
A;Superfamily: tumor necrosis factor
C;Keywords: tumor
A;Note: the authors translated codon CTC for residue 172 as Ile
A;Comment: This protein is structurally related pleiotropic cytokine with overlappi

```
Query Match             13.5%;  Score 205;  DB 1;  Length 202;
Best Local Similarity   32.9%;  Pred. No. 4.2e-08;
Matches   51;  Conservative  27;  Mismatches  67;  Indels  10;  Gaps  2;

Qy  137 PPEKK-----ELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFYV  192
        ::| |     : | : : ||:  :  :   ||  ||   |::| ||| |  |:|| ||
Db   48 PPQKHLTHGLLKPAAHLVGYPSKQNSLLWRANTDRAFLRHGFSLNNNSLLIPTSGLYFVY  107

Qy  193 SKVYFRGQSCN-------NLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLG  246
        ||||:| ||:|       :   | |: :      |  :::    :||      ||  | |
Db  108 SQVVFSGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLLSAQKSVYPGLQGPWVRSMYQG  167

Qy  247 AVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL  281
        ||| |:   : | :: :  :|::| |  ||| |:|
Db  168 AVFLLSKGDQLSTHTDGISHLHFSPSTVFFGAPAL  202
```

RESULT 5
B27303
tumor necrosis factor beta precursor - mouse
N;Alternate names: lymphotoxin; TNF beta

C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
A;Accession: B27303; S01342; S10083; I56004; I48853; I55980
A;Molecule type: DNA
A;Residues: 1-202 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831
R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R.S
Nucleic Acids Res. 14, 7713-7725, 1986
A;Accession: S10083; MUID:89145562; PMID:3147435
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Molecule type: mRNA
A;Residues: 6-202 <WEI>
A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned
A;Reference number: I56004; MUID:87252204; PMID:2885372
A;Accession: I56004
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:Y00137; NID:g54842; PIDN:CAA68330.1; PID:g54843
, C.
Immunol. 138, 4496-4501, 1987
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: I55980; MUID:87224127; PMID:2884262
A;Accession: I55980
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-202 <RE3>
A;Accession: I48853
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:Y00137; NID:g54842; PIDN:CAA68330.1; PID:g54843

R;Gray, P.W.; Chen, E.Y.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A;Reference number: I48853; MUID:87231097; PMID:3588316
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A;Accession: I48853; MUID:87231097; PMID:3588316
A;Cross-references: GB:M17015; NID:g198880; PIDN:AAA39450.1; PID:g387407
R;Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedo
Mol. Biol. (Mosk.) 23, 1743-1750, 1989
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31483.1; PID:g165755;
A;Residues: 1-197 <SH>

Oncogene Res. 3, 409-414, 1988
A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by
R;Weil, D.; Dautry, F.
A;Cross-references: EMBL:X06217
A;Residues: 1-11,139-160,'CG','163-178 <NED>
A;Residues: 1-11,139-160 'CG',163-178 <NED>
Residues: 1-11,139-160 'CG',163-178 <NED>
A;Cross-references: S01342
A;Reference number: S01342
Gene 95, 215-221, 1990
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are
A;Accession: S01342; MUID:87040736; PMID:3490653
A;Molecule type: DNA
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec
Nucleic Acids Res. 15, 9083-9084, 1987
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
A;Cross-references: B27303; S01342; S10083; I56004; I48853; I55980
A;Accession: B27303
A;Molecule type: DNA
A;Residues: 1-202 <SEM>

RESULT 6

JH0309
tumor necrosis factor beta precursor - rabbit
N;Alternate names: lymphotoxin; TNF beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: JH0309; PN0098
A;Title: Cloning and structural analysis of the genes, coding for rabbit tumor necros
A;Reference number: PN0098; MUID:90220566; PMID:2633043
A;Accession: PN0098
A;Molecule type: mRNA
A;Residues: 1-197 <SHA>
A;Cross-references: GB:X55745; NID:g297167; PIDN:CAA39275.1; PID:g297168
C;Genetics:
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; glycoprotein; lymphokine; macrophage
C;Introns: 25/3; 61/1
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-197/Product: lymphotoxin #status predicted <MAT>

Query Match   13.1%;   Score 200;   DB 1;   Length 197;
Best Local Similarity 26.0%;   Pred. No. 9.6e-08;
Matches   61;   Conservative 28;   Mismatches   82;   Indels   64;   Gaps   7;

Qy   55 PPPPPPPLPPLPPLPPLPPLKKRGNHSTGLCLIVMFMVLVALVGLGMFQLFHLQKELAEL 114
            |||| :| | |||
Db   19 PPPPGAQGLPGAEFPPSAAR--- 38

Qy   115 RESTSQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSG 173
            || :| | |:   : |:||| || | ||| |
Db   39 -------NAQORLQKHFGHST----------LKPAAHLVGDPSAQD-SLRWRANTDRAFLRHG 83

Qy   174 VAYKKGGLVINETGLIYFVYSKYYFRGQSCN-----------NLPLSHKVYMNNSKYPQDLVNMEG 227
            |:   :||||||| || |:||: | | ||:||: | ||| || :
Db   84 FSLSNNSLLVPSSGLIYFYSQVVFSGECSPRAVPTTPLYLAHEVQLFSSQYSFHVPLLSA 143

Qy   228 KMMSYCTTGQ-MWARSSYLGAVFNLTSADHLIYVNVSELSLVNFEESQTFFGLYKL 281
            : ||||||| ||||| | || || | ||:|| :|| | | :: || :
Db   144 Q-KSVCPGQGPWVRSVYQGAVFLLTQGDQLSTHTDGIAHLLLSPSSVFFGAFAL 197

RESULT 7

QWHUX
lymphotoxin alpha precursor - human
N;Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C;Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01645;
R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goedd
J. Cell. Biochem. 29, 171-181, 1985
A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
A;Accession: A92755
A;Molecule type: DNA
A;Residues: 1-59, 'N', 61-205 <NED>
R;Iris, F.J.M.; Bouguéleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju
Nature Genet. 3, 137-145, 1993

Qy   245 LGAVFNLTSADHLIYVNVSELSLVNFEESQTFFGLYKL 281
            |||| || :| || :| | : | ||| || |
Db   166 QGAVFLLSKGDQLSTHTDGISHLHFSPSSVFFGAFAL 202

Query Match   13.4%;   Score 204;   DB 1;   Length 202;
Best Local Similarity 32.5%;   Pred. No. 5e-08;
Matches   51;   Conservative 25;   Mismatches   73;   Indels   8;   Gaps   2;

Qy   133 HPSPPPEKKE--LRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVRVKKGGLVINETGLYF 190
            || :: ||| ::| |: :: || || ||:| |||||| ||| :|||
Db   46 HPLPQKHLIHGILKPAAHLVGYPSKQNSLLWRASTDRAFLRHGFSLSNNSLLPTSGLYF 105

Qy   191 VYSKYYFRGQSCN----------NLPLSHKVYMRNSKYPQDLVNMEGKKMMSYCTTGQMWARSSY 244
            |||:|| | | ::   ::|:| || || ::| | |: |: ||:| || ::|
Db   106 VYSQVVFSGESCSPRAIPTTYILAHEVQLFSSQYPFHVPLLSAQKSVYPGLQGPWVRSMY 165

A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:9272029; PMID:8499047
A:Accession: S36154
A:Molecule type: nucleic acid sequence not shown; translation not shown
A:Residues: 1-12,'R',14-205 <IRI>
A:Molecule type: DNA
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
R:Immunogenetics 33, 50-53, 1991
A:Title: Haplotypic polymorphisms of the TNFB gene.
A:Reference number: I54482; MUID:91191175; PMID:1671667
A:Accession: I54482
A:Residues: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-124,'P',126-205 <RES>
A:Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A:Experimental source: ancestral haplotype 57.1
A:Note: 59-Asn was also found (ancestral haplotype 8.1)
R:Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
R:Nature 312, 721-724, 1984
A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
cession: A93350
A:Reference number: A93350; MUID:85086243; PMID:6334807
lecule type: mRNA
A:Residues: 1-205 <GRA>
A:Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
R:Experimental source: lymphoblastoid cell line RPMI-1788
R:Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Nedwin, G.E.; Palladino, M.A.;
R:Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A:Title: Tumor necrosis factors: gene structure and biological activities.
A:Reference number: A32877; MUID:87217059; PMID:3472740
A:Accession: B32877
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 35-205 <GOE>
R:Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A:Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hy
A:Reference number: A91906; MUID:87057135; PMID:3536896
A:Accession: A91906
A:Molecule type: mRNA
A:Residues: 1-59,'N',61-205 <KOB>
A:Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A:Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue
R:Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: A61478
A:Molecule type: protein
A:Residues: 56-79,86-95,'X',97,'X',99,119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1
oigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
EBS Lett. 314, 85-88, 1992
A:Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatio
A:Reference number: S26951; MUID:93083656; PMID:1451807
A:Accession: S26951
A:Molecule type: protein
A:Residues: 35-59,'N',61-205 <VOI>
R:Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A:Note: 60-Thr was also found
A:Note: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
A:Reference number: S34742; MUID:93311995; PMID:8323280
A:Contents: annotation
C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
while having no detrimental effect on normal cells. It can also act synergistically wit
C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
ical activities but are produced by different cell types and have different induction ki
C:Genetics:
A:Gene: GDB:LTA; LT; TNFB
A:Cross-references: GDB:120442; OMIM:153440
A:Map position: 6p21.3-6p21.3

A:Introns: 33/3; 69/1
A:Note: the first intron occurs before the initiator codon
C:Superfamily: tumor necrosis factor
C:Keywords: cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-205/Product: lymphotoxin #status predicted <MAT>
F:41/Binding site: carbohydrate (Thr) (partial) #status experimental
F:96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   12.5%;   Score 191;   DB 1;   Length 205;
Best Local Similarity   27.4%;   Pred. No. 4.6e-07;
Matches   57;   Conservative   33;   Mismatches   90;   Indels   28;   Gaps   4;

```
Qy   81 LCLLVMFFMVLVALVGL-GLGMFQLEHLQKELAELRESTSQMHTASSLEKQIGHPSPPE 139
            ||  |    .: |     |  ||  |      .|||  |    ::|   | |||
Db   19 LLLLGLLILVLLPGAQGLPGVG------LTPSAAQTARQHPKMHLAHS----------- 59

Qy  140 KKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKRGGLVINETGLYFVYSKVYFRG 199
         ||  :     ||:| :|||||||  |||  |.||| ||||||||||| |:|||:|| |||
Db   60 --TLKPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSG 117

Qy  200 Q------SCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTS 253
         |       :| ||||||||||||||||||||||||| ||.|  ||||||||||||||||
Db  118 KAYSPKATSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQ 177

Qy  254 ADHLIYVNVSELSLVNFEESQTFFGLYKL 281
         |||||| ||||:|| ::|| ||||||||
Db  178 GDQLSTHTDGIPHLVLSPSTVFFGAFAL 205
```

RESULT 8

JQ1344

tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi
A:Reference number: JQ1344; MUID:92084125; PMID:1748301
A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>
A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match   12.2%;   Score 186.5;   DB 1;   Length 234;
Best Local Similarity   27.2%;   Pred. No. 1.1e-06;
Matches   62;   Conservative   36;   Mismatches   99;   Indels   31;   Gaps   10;

```
Qy   72 KKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQOLFHL-------OKELAELRESTSQMHTA 124
            |      | | ||:|||||:| ||| |  |  |      | :|||  |||  | |
Db   20 RAGGPQGSRRCLCLSLFSFL--LVAGATTLFCLLHFGVIGPQOREGOLPNAFQSINPL--A 75

Qy  125 SSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEW-EDTYGIVLLSGVKYKRGGLVI 183
          ::|   ||  | |||  :||||||||||  || ||||  ||||||| ||||||||||||
Db   76 QTLRSSSRTPSDKP------VAHVVANPQAEQO-LQWLSGRANALLANGVKLTDNQLVV 127

Qy  184 NETGLYFVYSKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTT------ 235
          ||||||||||||||||       |||||||||||||||||||||||||||||||
Db  128 PLDGLYLIYSQVLFKGQGCPSTHVLLITHTISRLAVSYPSKVNLLSA-IKSPCHTESPEQA 186

Qy  236 -GQMWARSSYLGAVFNLTSADHLIYVNVSELSLVNFEES-QTFFGLYKL 281
```

RESULT 9

Db   S12606

187 EAKPWYEPIYLGGVFQLEKGDQLSAEINQPNVILDFAESGQVYFGIIAL 234
     | | ||| ||:| |:|| ::| |: || ::|| || ::||| |

Db   187 EAKPWYEPIYLGGVFQLEKGDQLSAEINQPNVILDFAESGQVYFGIIAL 234

S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S12790; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17290; MUID:91340150; PMID:1874444
A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KUH>
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

Query Match   12.2%;   Score 185.5;   DB 1;   Length 232;
Best Local Similarity   28.7%;   Pred. No. 1.3e-06;
Matches   68;   Conservative   26;   Mismatches   92;   Indels   51;   Gaps   10;

Qy   72 KKRGNHSTGLCLLVMFPMVLVALVGLGMFQLFHL------QKE--------LAELR 115
        || : : | || | | |:|| :| || | || || |
Db   20 KAGGPQGSRRCLCLSLFSFL--LVAGATTLFCLLHFEVIGPQKEEFPAGPLSINPLAQGL 77

Qy   116 ESTSQMHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGV 174
         | |::| :|| | | |||:||| | ||:|| :| | || | || |
Db   78 RSSQTSD------------------KPVAHVANVKAEGQ-LQWQSGYANALLANGV 116

Qy   175 KYKKGLVINETGLYFVYSKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMEGKKMMSY 232
         | | |:: ::|:| || :||| | : | || ||| |:||:|| :||| | ||
Db   117 KLKDNQLVVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIAVSY-QTKVNLLSAIKSP 175

Qy   233 C------TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFGLYKL 281
         : || | | ||| || | |::| ||| |:   :|:|| |: || |
Db   176 CQRETPEGAEARPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL 232

RESULT 10

S17289
tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S17289
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17289
A;Molecule type: DNA
A;Residues: 1-204 <KUH>
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133
C;Genetics:
A;Introns: 32/3; 68/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match   12.1%;   Score 184;   DB 1;   Length 204;
Best Local Similarity   32.7%;   Pred. No. 1.5e-06;
Matches   53;   Conservative   22;   Mismatches   75;   Indels   12;   Gaps   6;

Qy   130 QIGHPSPPPE--KKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSGVYKYKKGGLVINET 186
         || | | | | ||||||| | ||:|| :| | | || | ||| | | |||| |
Db   45 QPAHQHPPKHLARGTLKPAAHLVGDPSTPD-SLRWRANTDRAFLRHGFLLSNNSLLVPTS 103

Qy   187 GLYFVYSKVYFRGQSC------NNLPLSHKVYMRNSKYPQDLVMEGKKMMSYCTTGQ-MW 239
         ||||||:|:|||| |: | || ||| |:||:|| :||| | || ||| |
Db   104 GLYFVYSQVVFSGEGCFPRATPTLIYLAHEVQLFSSQYPEHVPLLSAQ-KSVCPGPGPW 162

Qy   240 ARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 281
          | | ||| ||:|:|:| ||| |: |:| |:| || |
Db   163 VRSVYQGAVFLLTQGCDQLSTHTDGTPHLLLSPSSVFFGAFAL 204

RESULT 11

S24641
lymphotoxin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I46046; S24641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46046
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-204 <CL2>
A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C;Genetics:
A;Introns: 32/3; 68/1
C;Superfamily: tumor necrosis factor

Query Match   12.0%;   Score 183.5;   DB 1;   Length 204;
Best Local Similarity   31.5%;   Pred. No. 1.6e-06;
Matches   62;   Conservative   27;   Mismatches   89;   Indels   19;   Gaps   8;

Qy   94 LVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEKQIGHPSPPP-EKKELRKVAHLTGK 152
        || | | |: | || |:| | || |:|| :|| | | ||||||| | ||
Db   18 LLLLGL---LLALPLEAQGLRGIGLTPSAAQPAHQOL----PFPFTRGTLKPAAHLVGD 69

Qy   153 SNSRSMPLEWE-DTYGIVLLSGVKKYKKGGLVINETGLYFVYSKVYFRGQSC------NNL 205
        |:|| :| | | | || | |||: || :| ||| ||||||:|:||||: | |||
Db   70 PSTQD-SLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPL 128

Qy   206 PLSHKVYMRNSKYPQDLVMEGKKMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSEL 264
        | || |:|||:|| :||| | || :||| | | ||| || |:|:| ||| |:
Db   206 ... PLSHKVYMRNSKYPQDLVMEGKKMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSEL 264

Db   129 YLAHEVQLFSPQPFHVPLLSAQ-KSVCPQGPGPWVRSVYQGAVPLLTRGDQLSTHTDGI 187

Qy   265 SLVNFEESQTFFGIYKL 281
         | | | ||| |
Db   188 SHLLLSPSSVFFGAPAL 204

RESULT 12
S24642
tumor necrosis factor alpha precursor - bovine
N:Alternate names: tumor necrosis factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: I46047; S24642
R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46047
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
C:Gene: TNFA
C:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match   12.0%; Score 183; DB 1; Length 233;
Best Local Similarity   29.4%; Pred. No. 2e-06;
Matches   65; Conservative 27; Mismatches 111; Indels 18; Gaps 8;

Qy   72 KKRGNHSTGLCLLVMFFMVLVALVLGLGMFQLFHLQKELAELRESTSQMHTASSLEKQI 131
         :|| | |: | ||| :|:|:||
Db   20 KAGGPQGRSCLCLSLFSFL--LVAGATTLFCLLHFGVIGPQREESPGGPSINSPLVQTL 77

Qy   132 GHPSPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVYKYKKGGLVINETGLYF 190
         | || || | | || | :|:|| | | :||: | ||| || | |: | || |
Db   78 RSSSQASSNK---PVAHVADINSPGQ-LRWWDSYANALMANGVKLEDNQLVPADGLYL 133

Qy   191 VYSKVYFRGQSCNNLP--LSHKVYMRNSKYPQDLVMMEGKMMSYC------TTGQMWAR 241
         :|| || ||| || |:| | ||||:: | | | | ||:|: |
Db   134 IYSQVLFRGQGCPSTPLFLTHTISRIAVSY-QTKVNILSAIKSPCHREPEWAEARKPWYE 192

Qy   242 SSTLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 281
         ||| || |||| |||| | | |:||||| ||| |||:
Db   193 PIYQGGVFQLEKGDRLSAEINLPDYLDYAESGQVFFGIYAL 233

RESULT 13
?JUN
tumor necrosis factor alpha precursor (validated) - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I5331l; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: GB:X02910; GB:X02159; NID:g937209; PIDN:CAA26669.1; PID:g937210
R:Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-233 <IRI>
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02159; NID:g937209; PIDN:CAA26669.1; PID:g937210
A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promy
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology t
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', 64-233 <WAN>
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.;
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;
R:Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashim
Eur. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and compari
A:Reference number: I5331l; MUID:86030296; PMID:3932069
A:Accession: I5331l
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAR>
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A:Experimental source: U-937 cells
R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:g544751
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
A:Reference number: A59163; MUID:93018820; PMID:1426651
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:85130974; PMID:3871770
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
ut are produced by different cell types and have different induction kinetics.
C:Genetics:
C:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1

C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match   11.9%;   Score 181;   DB 1;   Length 233;
Best Local Similarity   27.4%;   Pred. No. 2.9e-06;
Matches   61;   Conservative   32;   Mismatches   112;   Indels   18;   Gaps   8;

```
Qy   70  PLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEK 129
         | |:  :  | |:| |  | | |  |  :| |  || || :|:|:          | :
Db   18  PKKTGGPQGSRRCLFLSLFSFLI--VAGATTLFCLLHFGVIGPQREEPPRDLSLISPLAQ 75

Qy  130  QIGHPSPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGL 188
              | |  |:     |||       | | || |||||    || :|:||:|
Db   76  AVRSSSRTPSDK---PVAHVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGL 131

Qy  189  YFVYSKYYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC------TTGQMW 239
         |:|:|| :|| ::   |||:||       |:     |  || :|||        |||:|
Db  132  YLIYSQVLFKGQGCPSTHVLLTHTISRIAVSY-QTKVNLLSAIKSPCQRETPEGAEAKPW 190

Qy  240  ARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 281
         | :  ||| | |  |  | : |  |:||| |:   :|||:|
Db  191  YEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
```

RESULT 14
A34043
hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C;Species: Owenia fusiformis
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34043; B34043
R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized by the repetition o
A;Reference number: A90159; MUID:90147742; PMID:2105723
A;Accession: A34043
A;Molecule type: DNA
A;Residues: 1-141 <BAK>
Cross-references: GB:M32217
Accession: B34043
A;Molecule type: DNA
A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217

Query Match   11.6%;   Score 177;   DB 2;   Length 141;
Best Local Similarity   49.3%;   Pred. No. 3.2e-06;
Matches   35;   Conservative   6;   Mismatches   28;   Indels   2;   Gaps   1;

```
Qy   18  SASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPPLPPPPPPPLPPPLKKRGNH 77
         :  | || |   |||||||||||||| ||||||||||||||||  |:|||| :||||
Db    6  SLFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPRRARIHH 65

Qy   78  STGLCLLVMFF 88
         :|:|| :| ||
Db   66  N--IPLFLFFF 74
```

RESULT 15
S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S22052
R;Sanjawala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match   11.6%;   Score 176;   DB 1;   Length 233;
Best Local Similarity   27.8%;   Pred. No. 6.7e-06;
Matches   62;   Conservative   30;   Mismatches   113;   Indels   18;   Gaps   8;

```
Qy   70  PLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEK 129
         | |:  :  | |:| |  | | |  |  :| |  || || :|:|:          | :
Db   18  PKKTGGPQGSRRCLFLSLFSFL--LVAGATTLFCLLHFGVIGPQREEPKDPSLISPLAQ 75

Qy  130  QIGHPSPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGL 188
              | |  |:     |||       | | || |||||    || :|:||:|
Db   76  AVRSSSRTPSDK---PVAHVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGL 131

Qy  189  YFVYSKYYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC------TTGQMW 239
         |:|:|| :|| ::   |||:||       |:     |  || :|||        |||:|
Db  132  YLIYSQVLFKGQGCPSTHVLLTHTISRIAVSY-QTKVNLLSAIKSPCQRETPEGAEAKPW 190

Qy  240  ARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 281
         | :  ||| | |  |  | : |  |:||| |:   :|||:|
Db  191  YEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
```

Search completed: June 24, 2003, 11:08:51
Job time : 22.3505 secs

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